5040

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source:

Date Processed by STIC:

10/5/7,324

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 2023 1 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
 U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04



PCT

12/28/04

RAW SEQUENCE LISTING

DATE: 12/28/2004

PATENT APPLICATION: US/10/517,324

TIME: 11:50:05

Input Set : A:\040679.txt

```
Output Set: N:\CRF4\12282004\J517324.raw
      3 <110> APPLICANT: SinoGenoMax Company Ltd
      5 <120> TITLE OF INVENTION: Randomised DNA libraries and double-stranded RNA libraries,
use and
              method of production thereof
      8 <130> FILE REFERENCE: P06031PC00
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/517,324
C--> 11 <141> CURRENT FILING DATE: 2004-12-20
     13 <150> PRIOR APPLICATION NUMBER: US 60/390,108
     14 <151> PRIOR FILING DATE: 2002-06-21
                                                                 es Not Comply
     16 <160> NUMBER OF SEQ ID NOS: 45
                                                               Corpored Distatte North
     18 <170> SOFTWARE: PatentIn version 3.1
     20 <210> SEQ ID NO: 1
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     22 <212> TYPE: DNA
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                                                Pls explain source of gen
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     52 <220> FEATURE:
     53 <221> NAME/KEY: misc_feature
     54 <222> LOCATION: (7)..(7)
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     60 <221> NAME/KEY: misc feature
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   --62 <223 > OTHER INFORMATION: Represents nucleotides not clearly identified in the
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                                                          nutic response
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PS RAW SEOTIFME

DATE: 12/28/2004 TIME: 11:50:05

Input Set : A:\040679.txt

Output Set: N:\CRF4\12282004\J517324 raw

	Output Set: N:\CRF4\12282004\J517324.raw	
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M>	67 tccagmanc gcgggcccag tgtcactagg cgggaacacc cagcgcgcgt gcgccctggc	60
	69 aggaagatgg ctgtgaggga caggggagtg gcgcctgca atatttgcat gtcgctatgt	120
	71 gttctgggaa atcaccataa acgtgaaatg tctttggatt tgggaatctt ataagttctg	180
	73 tatgagacag atcttcaata ttggccatta gccatattat tcattggtta tatagcataa	240
	75 atcastattg gctattggcc attgcatacg ttgtatctat atcatastat gtacatttat	300
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. •	91 <220> FEATURE:	
	92 <223> OTHER INFORMATION: 5? rimer 94 <400> SEQUENCE: 4	
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	131 ccccaagett aaaaatgtte ttgatteatt tatttttta gatetteece	50
	134 <210> SEQ ID NO: 8	^
	135 (Z11) LENGTH: 50	
	137 (212) OBCANISM Artificial Comment What I S The Sou	(ree on
	139 (220) EPATIDE:	atic material.
	140 <223 OTHER INFORMATION (10 miglestides mendenical services)	acric
	142 <220 FEATURE:	· /
	143 <221> NAME/KEY: misc feeture	d
	143 (221) MANUAL MISC_TEACUTE	
	$ \mathcal{M}$ \mathcal{M} \mathcal{M}	XX FE
•	\mathcal{C}^{3}	_
	134 <210> SEQ ID NO: 8 135 <211> LENGTH: 50 136 <212> TYPE: DNA 137 <213> ORGANISM: Artificial Sequence What IS the South 139 <220> FEATURE: 140 <223> OTHER INFORMATION: 19 nucleotides randomized region 142 <220> FEATURE: 143 <221> NAME/KEY: misc_feature C:\CRF4\OUTHOLD\VsrJ517324.htm	A 11 ~ -
		M 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	$\sim 1 \leq PP $ 1tt	VV 1-11
		-, choi
file://C	:\CRF4\OUTHOLD\VsrJ517324.htm	CI MAIN W Y12/12/01
	12.1 I/Y I/X	7 1A FVITT / 12/20/04

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/517,324

DATE: 12/28/2004 TIME: 11:50:05

Input Set : A:\040679.txt

Output Set: N:\CRF4\12282004\J517324.raw 144 <222> LOCATION: (17)..(35) 145 <223> OTHER INFORMATION: Randomized region 148 <400> SEQUENCE: 8 W--> 149 ggggaagate taaaaahnnn nnnnnnnn nnnnhttttt aagettgggg S explain "1) "locations 152 <210> SEQ ID NO: 9 153 <211> LENGTH: 51 154 <212> TYPE: DNA 155 <213> ORGANISM: (Artificial Sequence) Source of Genetic Maderial,
157 <220> FEATURE: PIS explain Source of Genetic Maderial, PIS explain 158 <223> OTHER INFORMATION: 20 nucleotides randomized region 160 <220> FEATURE: 161 <221> NAME/KEY: misc feature represent à single Muleotide 162 <222> LOCATION: (17)..(36) 163 <223 > OTHER INFORMATION: Randomized region. 166 <400> SEQUENCE: 9 W--> 167 ggggaagate taaaaaannn nnnnnnnn nnnnnntttt taagettggg g 170 <210> SEQ ID NO: 10 171 <211> LENGTH: 52 172 <212> TYPE: DNA 173 <213> ORGANISM: Artificial Sequence 175 <220> FEATURE: 176 <223> OTHER INFORMATION: (21 nucleotides randomized region 178 <220> FEATURE: 179 <221> NAME/KEY: misc feature Same errors 180 <222> LOCATION: (17)..(37) 181 <223 > OTHER INFORMATION: (Randomized region. 184 <400> SEQUENCE: 10 W--> 185 ggggaagate taaaaamnnn nnnnnnnnn nnnnnnnttt ttaagettgg gg 52 188 <210> SEQ ID NO: 11 189 <211> LENGTH: 15 190 <212> TYPE: DNA 191 <213> ORGANISM: Artificial Sequence 193 <220> FEATURE: 194 <223> OTHER INFORMATION: primer 196 <400> SEQUENCE: 11 197 ccccaagctt aaaaa 15 200 <210> SEQ ID NO: 12 '201 <211> LENGTH: 19 202 <212> TYPE: DNA 203 <213> ORGANISM: Artificial Sequence 205 <220> FEATURE: 206 <223> OTHER INFORMATION: 19 base pair clone

217 <220> FEATURE:

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212 <210> SEQ ID NO: 13 213 <211> LENGTH: 19 214 <212> TYPE: DNA

215 <213> ORGANISM: Artificial Sequence

19

RAW SEQUENCE LISTING DATE: 12/28/2004 PATENT APPLICATION: US/10/517,324 TIME: 11:50:05

Input Set : A:\040679.txt

Output Set: N:\CRF4\12282004\J517324.raw

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290	<223> OTHER INFORMATION: 19 base pair clone	

RAW SEQUENCE LISTING DATE: 12/28/2004
PATENT APPLICATION: US/10/517,324 TIME: 11:50:05

)

Input Set : A:\040679.txt

Output Set: N:\CRF4\12282004\J517324.raw

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                                                       Same errors
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     363 <211> LENGTH: 35
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RAW SEQUENCE LISTING ERROR SUMMARY PATENT APPLICATION: US/10/517,324

DATE: 12/28/2004 TIME: 11:50:06

Input Set : A:\040679.txt

Output Set: N:\CRF4\12282004\J517324.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 7,9 V Seq#:8; N Pos. 17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35 Seq#:9; N Pos. 17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36 Seq#:10; N Pos. 17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36 Seq#:10; N Pos. 37 Seq#:24; N Pos. 17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35 Seq#:25; N Pos. 11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29 Seq#:26; N Pos. 7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25 Seq#:34; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19 Seq#:38; N Pos. 8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,36 Seq#:38; N Pos. 37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54 Seq#:39; N Pos. 4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,32,33,34 Seq#:39; N Pos. 35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50 Seq#:42; N Pos. 8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26 Seq#:43; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19 Seq#:44; N Pos. 4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22 Seq#:45; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/517,324

DATE: 12/28/2004 TIME: 11:50:06

Input Set : A:\040679.txt

Output Set: N:\CRF4\12282004\J517324.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
L:583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:627 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER.
ATTN: NEW RULES CASE	SERIAL NUMBER: 13 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Wrapped Nucleie	DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY
Wrapped Aminos	The numberitext at the end of each line "wrapped" down to the next line. This may occur if your file prevent "wrapping."
	The rules require that a line not exceed 72 characters in length. This includes white spaces.
JMisaligned Amino	The australian and exceed 12 characters in length. This includes white spaces
Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers:
4Non-ASCII	The submitted file
- .	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
SVariable Length	Scource (4)
	Sequence(s) contain n's or Xaa's representing more than one sessidue. Per Sequence Rules, residue having variable length and single residue. Please present the maximum
•	cach n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing
GPatentin 2.0	A "bue" in Paracet
306	sequences(e) con as caused the <220>.<221> section as t
F	Normally, Patentln would automatically generate this section from the subsequent amino acid sequence. Please manually copy the relevant <220>-<223> section from the subsequent amino acid sequence. This applies to the mandatory <220>-<223> section to
() A	he subsequent amino acid sequence. This applies to the month of relevant <220><221> section from the
) 0.	equences.
Seviated Seducuces 2	Cquence(s)
(120 (0223)	1) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown) 1) SEQUENCE CHARACTERISTICS (Do not insert sex)
(, (x	SEQUENCE CHARACTERISTICS (Do not insert any cold as shown)
Th	SEQUENCE CHARACTERISTICS (Do not insert any sublicatings under this licating) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
D.	A is shown)
	Pucnce(s)
8 Skipped Sequences Sec	Juance(s) - acopolitics a response to include the skillbed sequences
(0.4 (00003) 531	10> scovence and a mitentional please insert the following to
<40 000	00> sequence id number
Oscorns or Xaa's Usc	of n's and/or X >> - 1
(NEW RULES) Per	of n's and/or X22's have been detected in the Sequence Listing
In c	1 82) of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present 220> to <223> section, please explain location of n or Xaa, and which resid
Per 1	823 of Seguera of X22 represents
Response scien	1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence or tific all Sequence or tificial Sequence or tificial Sequence
15 An	tificial Sequence Rules, the only valid ! > responses are Unknown, Artificial Sequence or tificial Sequence or tificial Sequence.
,	
Usco	1 <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or Federal Register, "Orio/1998, Vol. 63
" <u>Unk</u>	nown." Please explain source of second (211) "Organism" response is "Antheral C
(360)	nown." Please explain source of genetic material in <220> to <221> section. Federal Register, "Orio1/1998, Vol. 63, No. 104, pp. 29631, 2976
I alentin 2.0 Picase	do not use "C: (Sec. 1.82) of Sequence Rules)
	NE IN MILLION - I TAICHIN VELLION AND THE TAICHIN THE
listing	Instead, please use "File Manaper" or any other
Misusc of NX22 "n" car	Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
	material: "Xaa" can only represent a single amin
	AMC - Biotechnology C

AMC - Biotechnology Systems Branch - 09/09/2003